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SEQUENCE LISTING

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<120> Plant production of immunoglobulins with reduced fucosylation

<130> 38136-5001-WO

<150> US 60/429,385

<151> 2002-11-27

<160> 85

<170> PatentIn version 3.1

<210> 1

<211> 1494

<212> DNA

<213> Herpes simplex virus

<220>

<221> CDS

<222> (1) .. (1494)

<223>

<220>

<221> misc_feature

<223> HSV Heavy Chain sequence

<400> 1

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1 5 10 15	
gtc cat tgc cag gtt cag ctc gtg cag tca ggt gct gag gtg aag aag	96
Val His Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20 25 30	
cct ggc tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggt tcc ttc	144
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe	
35 40 45	
agc tcc tat gct atc aac tgg gtg agg caa gct cct gga caa ggg ctt	192
Ser Ser Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
50 55 60	
gag tgg atg gga ggg ctc atg cct atc ttt ggg aca aca aac tac gcg	240
Glu Trp Met Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala	

65	70	75	80	
cag aag ttc cag gac agg ctc acg att acc gcg gac gta tcc acg agt Gln Lys Phe Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser 85 90 95				288
aca gcc tac atg caa ctg agc ggc ctg aca tat gaa gac acg gcc atg Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met 100 105 110				336
tat tac tgt gcg aga gtt gcc tac atg ctt gaa cct acc gtc act gca Tyr Tyr Cys Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala 115 120 125				384
ggg ggt ttg gac gtc tgg ggc caa ggg acc ttg gtc acc gtc tcc tcc Gly Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser 130 135 140				432
gca tcc ccg acc agc ccg aag gtc ttc ccg ctg agc ctc tgt agc acc Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr 145 150 155 160				480
cag cca gat ggg aac gtg gtc atc gcc tgc ctg gtc cag ggc ttc ttc Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe 165 170 175				528
cct cag gag cca ctc agt gtg acc tgg agc gaa agc gga cag ggc gtg Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val 180 185 190				576
acc gcc agg aac ttc cca ccc agc cag gat gcc tcc gga gac ctg tac Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr 195 200 205				624
acc acg tcc agc cag ctg acc ctt ccg gcc aca cag tgc cta gcg ggc Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly 210 215 220				672
aag tcc gtg aca tgc cac gtg aag cac tac acg aat ccc agc cag gat Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp 225 230 235 240				720
gtg act gtg ccc tgc cca gtt ccc tca act cca cct acc cca tct ccc Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro 245 250 255				768
tcg act cca cct acc cca tct ccc tca tgc tgc cac ccc agg ctg tca Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser 260 265 270				816
ctg cac agg cct gcc ctc gag gac ctg ctc tta ggt tcg gaa gcg aac Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn 275 280 285				864
ctc acg tgc aca ctc acc ggc ctg aga gat gcg tca ggt gtc acc ttc Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe 290 295 300				912
acc tgg acg ccc tca agt ggt aag agc gct gtt caa ggc cca cct gag Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu 305 310 315 320				960

cgt gac ctc tgt ggc tgc tac agc gtg tcc agt gtc ctt ccg ggc tgt 1008
 Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
 325 330 335

gcc gag cct tgg aat cat ggg aag acc ttc act tgc act gct gcc tac 1056
 Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
 340 345 350

ccc gag agc aag acc ccg cta acc gcc acc ctc tcg aaa tcc ggc aac 1104
 Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn
 355 360 365

aca ttc cgg ccc gag gtc cac ctg ctg ccg ccg ccg tcg gag gag ctg 1152
 Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Ser Glu Glu Leu
 370 375 380

gcc ctg aac gag ctg gtg acg ctg acg tgc ctg gcg cgc ggc ttc agc 1200
 Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser
 385 390 395 400

ccc aag gac gtg ctg gtt cgc tgg ctg cag gcc tca cag gag ctg cct 1248
 Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro
 405 410 415

agg gag aag tac ctg act tgg gca tcc ccg cag gag ccc agc caa ggc 1296
 Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly
 420 425 430

acc acc acc ttc gct gtg acc tcg ata ctg cgc gtg gca gcc gag gac 1344
 Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp
 435 440 445

tgg aag aag ggt gac acc ttc tcc tgc atg gtg ggc cac gag gcc ctt 1392
 Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu
 450 455 460

ccg ctg gcc ttc aca cag aag acc atc gac cgc ttg gcg ggt aaa ccc 1440
 Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro
 465 470 475 480

acc cat gtc aat gtg tct gtt gtc atg gcg gag gtg gac ggc acc tgc 1488
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 485 490 495

tac tga 1494
 Tyr

<210> 2
 <211> 497
 <212> PRT
 <213> Herpes simplex virus

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Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe
 35 40 45
 Ser Ser Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60
 Glu Trp Met Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala
 65 70 75 80
 Gln Lys Phe Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser
 85 90 95
 Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met
 100 105 110
 Tyr Tyr Cys Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala
 115 120 125
 Gly Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 130 135 140
 Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr
 145 150 155 160
 Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
 165 170 175
 Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
 180 185 190
 Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
 195 200 205
 Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
 210 215 220
 Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
 225 230 235 240
 Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro
 245 250 255
 Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser
 260 265 270
 Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn
 275 280 285
 Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe
 290 295 300
 Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu
 305 310 315 320
 Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
 325 330 335
 Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
 340 345 350
 Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn

355 360 365
 Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu
 370 375 380
 Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser
 385 390 395 400
 Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro
 405 410 415
 Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly
 420 425 430
 Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp
 435 440 445
 Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu
 450 455 460
 Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro
 465 470 475 480
 Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys
 485 490 495

Tyr

<210> 3
 <211> 57
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Heavy chain signal peptide

<220>
 <221> CDS
 <222> (1)..(57)
 <223>

<400> 3
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 gtc cat tgc
 Val His Cys 57

<210> 4
 <211> 19
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Heavy chain signal peptide

<400> 4

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
 1 5 10 15

Val His Cys

<210> 5
 <211> 1368
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Mature heavy chain sequence

<220>
 <221> CDS
 <222> (1) .. (1368)
 <223>

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 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

tcg gtg aag gtc tcc tgc aag gct tct gga ggt tcc ttc agc tcc tat 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Ser Tyr
 20 25 30

gct atc aac tgg gtg agg caa gct cct gga caa ggg ctt gag tgg atg 144
 Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

gga ggg ctc atg cct atc ttt ggg aca aca aac tac gcg cag aag ttc 192
 Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

cag gac agg ctc acg att acc gcg gac gta tcc acg agt aca gcc tac 240
 Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser Thr Ala Tyr
 65 70 75 80

atg caa ctg agc ggc ctg aca tat gaa gac acg gcc atg tat tac tgt 288
 Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

gcg aga gtt gcc tac atg ctt gaa cct acc gtc act gca ggt ggt ttg 336
 Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala Gly Gly Leu
 100 105 110

gac gtc tgg ggc caa ggg acc ttg gtc acc gtc tcc tcc gca tcc ccg 384
 Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro
 115 120 125

acc agc ccg aag gtc ttc ccg ctg agc ctc tgt agc acc cag cca gat 432
 Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr Gln Pro Asp
 130 135 140

ggg aac gtg gtc atc gcc tgc ctg gtc cag ggc ttc ttc cct cag gag 480
 Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe Pro Gln Glu
 145 150 155 160

cca ctc agt gtg acc tgg agc gaa agc gga cag ggc gtg acc gcc agg 528

Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val Thr Ala Arg	
165 170 175	
aac ttc cca ccc agc cag gat gcc tcc gga gac ctg tac acc acg tcc	576
Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser	
180 185 190	
agc cag ctg acc ctt ccg gcc aca cag tgc cta gcg ggc aag tcc gtg	624
Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly Lys Ser Val	
195 200 205	
aca tgc cac gtg aag cac tac acg aat ccc agc cag gat gtg act gtg	672
Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp Val Thr Val	
210 215 220	
ccc tgc cca gtt ccc tca act cca cct acc cca tct ccc tcg act cca	720
Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro	
225 230 235 240	
cct acc cca tct ccc tca tgc tgc cac ccc agg ctg tca ctg cac agg	768
Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg	
245 250 255	
cct gcc ctc gag gac ctg ctc tta ggt tgc gaa gcg aac ctc acg tgc	816
Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys	
260 265 270	
aca ctc acc ggc ctg aga gat gcg tca ggt gtc acc ttc acc tgg acg	864
Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr	
275 280 285	
ccc tca agt ggt aag agc gct gtt caa ggc cca cct gag cgt gac ctc	912
Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu Arg Asp Leu	
290 295 300	
tgt gcc tgc tac agc gtg tcc agt gtc ctt ccg ggc tgt gcc gag cct	960
Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro	
305 310 315 320	
tgg aat cat ggg aag acc ttc act tgc act gct gcc tac ccc gag agc	1008
Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser	
325 330 335	
aag acc ccg cta acc gcc acc ctc tcg aaa tcc ggc aac aca ttc cgg	1056
Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg	
340 345 350	
ccc gag gtc cac ctg ctg ccg ccg ccg tcg gag gag ctg gcc ctg aac	1104
Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn	
355 360 365	
gag ctg gtg acg ctg acg tgc ctg gcg cgc ggc ttc agc ccc aag gac	1152
Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp	
370 375 380	
gtg ctg gtt cgc tgg ctg cag ggc tca cag gag ctg cct agg gag aag	1200
Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys	
385 390 395 400	
tac ctg act tgg gca tcc ccg cag gag ccc agc caa ggc acc acc acc	1248
Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr	

405	410	415	
ttc gct gtg acc tcg ata ctg cgc gtg gca gcc gag gac tgg aag aag			1296
Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys			
420	425	430	
ggt gac acc ttc tcc tgc atg gtg ggc cac gag gcc ctt ccg ctg gcc			1344
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala			
435	440	445	
ttc aca cag aag acc atc gac cgc			1368
Phe Thr Gln Lys Thr Ile Asp Arg			
450	455		

<210> 6
 <211> 456
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Mature heavy chain sequence

<400> 6
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
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 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Ser Tyr
 20 25 30
 Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala Gly Gly Leu
 100 105 110
 Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro
 115 120 125
 Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr Gln Pro Asp
 130 135 140
 Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe Pro Gln Glu
 145 150 155 160
 Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val Thr Ala Arg
 165 170 175
 Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser
 180 185 190
 Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly Lys Ser Val

195	200	205
Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp Val Thr Val 210 215 220		
Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro 225 230 235 240		
Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg 245 250 255		
Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys 260 265 270		
Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr 275 280 285		
Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu Arg Asp Leu 290 295 300		
Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro 305 310 315 320		
Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser 325 330 335		
Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg 340 345 350		
Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn 355 360 365		
Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp 370 375 380		
Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys 385 390 395 400		
Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr 405 410 415		
Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys 420 425 430		
Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala 435 440 445		
Phe Thr Gln Lys Thr Ile Asp Arg 450 455		

<210> 7
 <211> 69
 <212> DNA
 <213> Artificial sequence

<220>
 <223> heavy chain tailpiece

<220>
 <221> CDS

<222> (1)..(69)

<223>

<400> 7

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Leu	Ala	Gly	Lys	Pro	Thr	His	Val	Asn	Val	Ser	Val	Val	Met	Ala	Glu	
1				5					10					15		

gtg	gac	ggc	acc	tgc	tac	tga										69
Val	Asp	Gly	Thr	Cys	Tyr											
				20												

<210> 8

<211> 22

<212> PRT

<213> Artificial sequence

<220>

<223> heavy chain tailpiece

<400> 8

Leu	Ala	Gly	Lys	Pro	Thr	His	Val	Asn	Val	Ser	Val	Val	Met	Ala	Glu	
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Val	Asp	Gly	Thr	Cys	Tyr											
				20												

<210> 9

<211> 702

<212> DNA

<213> Herpes simplex virus

<220>

<221> CDS

<222> (1)..(702)

<223>

<220>

<221> misc_feature

<223> HSV light chain sequence

<400> 9

atg	gga	tgg	tcc	tgg	atc	ttt	ctc	ttc	ctt	ctg	tca	gga	gct	gca	ggt	48
Met	Gly	Trp	Ser	Trp	Ile	Phe	Leu	Phe	Leu	Ser	Gly	Ala	Ala	Gly		
1				5					10					15		

gtc	cac	tgc	gag	atc	gtg	ctc	acg	cag	tct	cca	ggc	acc	ctg	tct	ttg	96
Val	His	Cys	Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	
			20					25					30			

tgc	cca	ggg	gaa	cgt	gcc	acc	ctc	tcc	tgc	cgg	gcc	agt	cag	tcc	gtt	144
Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	
		35					40					45				

tcc	agc	gcg	tac	ctt	gcc	tgg	tac	cag	cag	aag	cct	ggc	caa	gct	ccc	192
Ser	Ser	Ala	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	
		50				55				60						

agg	ctc	ctc	atc	tat	ggg	gcg	tcc	agc	agg	gct	act	ggc	att	cca	gac	240
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Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp
 65 70 75 80
 cgc ttc tca ggc agt ggg tct ggg aca gac ttc acg ctc acc att agc 288
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95
 agg ctg gaa cct gag gat ttt gca gtg tac tac tgt cag cag tat ggt 336
 Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
 100 105 110
 cgc tca ccc acg ttc ggc cag ggg acc aag gtg gag atc aag cgc act 384
 Arg Ser Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 115 120 125
 gtg gct gca ccg tcg gtc ttc ata ttc ccg cca tcc gat gag cag ctg 432
 Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
 130 135 140
 aag tct ggc act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccg 480
 Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
 145 150 155 160
 aga gag gcg aag gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt 528
 Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
 165 170 175
 aac tcc caa gag tcc gtt aca gag cag gac agc aag gac agc acc tac 576
 Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
 180 185 190
 agc ctc agc aac acc ttg acg ctg agc aaa gcg gac tac gag aaa cac 624
 Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
 195 200 205
 aag gtc tac gcc tgc gaa gtc acc cat caa ggc ctg cgc tcg ccc gtc 672
 Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg Ser Pro Val
 210 215 220
 aca aag agc ttc aac cgg gga gag tgt tga 702
 Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> 10
 <211> 233
 <212> PRT
 <213> Herpes simplex virus

<400> 10
 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
 1 5 10 15
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 20 25 30
 Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
 35 40 45
 Ser Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 50 55 60

Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp
 65 70 75 80
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 85 90 95
 Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly
 100 105 110
 Arg Ser Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 115 120 125
 Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
 130 135 140
 Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
 145 150 155 160
 Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
 165 170 175
 Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
 180 185 190
 Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
 195 200 205
 Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg Ser Pro Val
 210 215 220
 Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230

<210> 11
 <211> 57
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Light chain signal peptide

<220>
 <221> CDS
 <222> (1)..(57)
 <223>

<400> 11
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 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
 1 5 10 15

48

gtc cac tgc
 Val His Cys

57

<210> 12
 <211> 19
 <212> PRT
 <213> Artificial sequence

<220>

<223> Light chain signal peptide

<400> 12

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
 1 5 10 15

Val His Cys

<210> 13

<211> 642

<212> DNA

<213> Artificial sequence

<220>

<223> Mature light chain sequence

<220>

<221> CDS

<222> (1)..(642)

<223>

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165

170

175

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 Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala Gly Gly Leu Asp Val
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<210> 19
 <211> 122
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 Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
 1 5 10 15

Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Ser Tyr Ala Ile Asn
 20 25 30

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Leu
 35 40 45

Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe Gln Asp Arg
 50 55 60

Leu Thr Ile Thr Ala Asp Val Ser Thr Ser Thr Ala Tyr Met Gln Leu
 65 70 75 80

Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg Val
 85 90 95

Ala Tyr Met Leu Glu Pro Thr Val Thr Ala Gly Gly Leu Asp Val Trp
 100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ala Ser
 115 120

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<220>
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<400> 20

Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly
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Leu Arg

<210> 21
<211> 18
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<220>
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<400> 21
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg

<210> 22
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> peptide tryptic fragment L-T2

<400> 22
Ala Thr Leu Ser Cys Arg
1 5

<210> 23
<211> 22
<212> PRT
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<220>
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<400> 23
Ala Ser Gln Ser Val Ser Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys
1 5 10 15

Pro Gly Gln Ala Pro Arg
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<210> 24
<211> 9
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<220>
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<400> 24
Leu Leu Ile Tyr Gly Ala Ser Ser Arg
1 5

<210> 25
<211> 7
<212> PRT
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<220>
<223> peptide tryptic fragment L-T5

<400> 25
Ala Thr Gly Ile Pro Asp Arg
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<210> 26
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<220>
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<400> 26
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
1 5 10 15

<210> 27
<211> 16
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<220>
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<400> 27
Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg
1 5 10 15

<210> 28
<211> 9
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<220>
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<400> 28
Ser Pro Thr Phe Gly Gln Gly Thr Lys
1 5

<210> 29
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<220>
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<400> 29

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

Leu Lys

<210> 30

<211> 16

<212> PRT

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<220>

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<400> 30

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
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<210> 31

<211> 4

<212> PRT

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<400> 31

Val Gln Trp Lys
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<210> 32

<211> 20

<212> PRT

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<220>

<223> peptide tryptic fragment L-T15

<400> 32

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
1 5 10 15

Gln Asp Ser Lys
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<210> 33

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T16

<400> 33

Asp Ser Thr Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys
1 5 10

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<220>
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<400> 34
Ala Asp Tyr Glu Lys
1 5

<210> 35
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<220>
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<400> 35
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg
1 5 10

<210> 36
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<220>
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<400> 36
Ser Pro Val Thr Lys
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<210> 37
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<220>
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<400> 37
Ser Phe Asn Arg
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<210> 38
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<220>
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<400> 38

Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp
1 5 10 15

Phe Thr Leu Thr Ile Ser Arg
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<210> 39

<211> 32

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<220>

<223> peptide tryptic fragment L-T6-7

<400> 39

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
1 5 10 15

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Arg
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<210> 40

<211> 13

<212> PRT

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Ser Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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<210> 41

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<400> 41

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
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Gln Leu Lys

<210> 42

<211> 19

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<223> peptide tryptic fragment L-T12-13

<400> 42

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
1 5 10 15

Glu Ala Lys

<210> 43

<211> 7

<212> PRT

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<220>

<223> peptide tryptic fragment L-T13-14

<400> 43

Glu Ala Lys Val Gln Trp Lys
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<210> 44

<211> 24

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T14-15

<400> 44

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
1 5 10 15

Ser Val Thr Glu Gln Asp Ser Lys
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<210> 45

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<223> peptide tryptic fragment L-T17-18

<400> 45

Ala Asp Tyr Glu Lys His Lys
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<210> 46

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment L-T18-19

<400> 46

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Arg
1 5 10

<210> 47
<211> 9
<212> PRT
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Ser Pro Val Thr Lys Ser Phe Asn Arg
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<210> 48
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Ser Phe Asn Arg Gly Glu Cys
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<210> 49
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<400> 49
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
1 5 10

<210> 50
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<212> PRT
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<400> 50
Lys Pro Gly Ser Ser Val Lys
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<210> 51
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<400> 51

Ala Ser Gly Gly Ser Phe Ser Ser Tyr Ala Ile Asn Trp Val Arg
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<210> 52

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<220>

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<400> 52

Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Leu Met Pro Ile
1 5 10 15

Phe Gly Thr Thr Asn Tyr Ala Gln Lys
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<210> 53

<211> 4

<212> PRT

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<400> 53

Phe Gln Asp Arg
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<210> 54

<211> 31

<212> PRT

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<220>

<223> peptide tryptic fragment H-T7

<400> 54

Leu Thr Ile Thr Ala Asp Val Ser Thr Ser Thr Ala Tyr Met Gln Leu
1 5 10 15

Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg
20 25 30

<210> 55

<211> 34

<212> PRT

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<220>

<223> peptide tryptic fragment H-T8

<400> 55

Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala Gly Gly Leu Asp Val
1 5 10 15

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro Thr Ser
20 25 30

Pro Lys

<210> 56
<211> 44
<212> PRT
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<220>
<223> peptide tryptic fragment H-T9

<400> 56
Val Phe Pro Leu Ser Leu Cys Ser Thr Gln Pro Asp Gly Asn Val Val
1 5 10 15

Ile Ala Cys Leu Val Gln Gly Phe Phe Pro Gln Glu Pro Leu Ser Val
20 25 30

Thr Trp Ser Glu Ser Gly Gln Gly Val Thr Ala Arg
35 40

<210> 57
<211> 30
<212> PRT
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<220>
<223> peptide tryptic fragment H-T10

<400> 57
Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser
1 5 10 15

Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly Lys
20 25 30

<210> 58
<211> 7
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<220>
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<400> 58
Ser Val Thr Cys His Val Lys
1 5

<210> 59
<211> 38
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<220>

<223> peptide tryptic fragment H-T12

<400> 59

His Tyr Thr Asn Pro Ser Gln Asp Val Thr Val Pro Cys Pro Val Pro
1 5 10 15

Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro
20 25 30

Ser Cys Cys His Pro Arg
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<210> 60

<211> 27

<212> PRT

<213> Artificial sequence

<220>

<223> peptide tryptic fragment H-T13

<400> 60

Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu
1 5 10 15

Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg
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<223> peptide tryptic fragment H-T14

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Asp Ala Ser Gly Val Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys
1 5 10 15

<210> 62

<211> 9

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<223> peptide tryptic fragment H-T15

<400> 62

Ser Ala Val Gln Gly Pro Pro Glu Arg
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<210> 63

<211> 23

<212> PRT

<213> Artificial sequence

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<223> peptide tryptic fragment H-T16

<400> 63

Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala
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Glu Pro Trp Asn His Gly Lys
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<210> 64

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Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser Lys
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<210> 65

<211> 9

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<223> peptide tryptic fragment H-T18

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Thr Pro Leu Thr Ala Thr Leu Ser Lys
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<210> 66

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<223> peptide tryptic fragment H-T19

<400> 66

Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser
1 5 10 15

Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg
20 25 30

<210> 67

<211> 5

<212> PRT

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<220>

<223> peptide tryptic fragment H-T20

<400> 67

Gly Phe Ser Pro Lys
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<210> 68
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<400> 68
Asp Val Leu Val Arg
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<400> 69
Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg
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<210> 70
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<223> peptide tryptic fragment H-T24

<400> 70
Tyr Leu Thr Trp Ala Ser Arg
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<210> 71
<211> 17
<212> PRT
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<400> 71
Gln Glu Pro Ser Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu
1 5 10 15

Arg

<210> 72
<211> 7
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<223> peptide tryptic fragment H-T26

<400> 72

Val Ala Ala Glu Asp Trp Lys

1 5

<210> 73

<211> 20

<212> PRT

<213> Artificial sequence

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<223> peptide tryptic fragment H-T28

<400> 73

Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala

1 5 10 15

Phe Thr Gln Lys

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<210> 74

<211> 4

<212> PRT

<213> Artificial sequence

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<223> peptide tryptic fragment H-T29

<400> 74

Thr Ile Asp Arg

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<210> 75

<211> 22

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<213> Artificial sequence

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<223> peptide tryptic fragment H-T30

<400> 75

Leu Ala Gly Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu

1 5 10 15

Val Asp Gly Thr Cys Tyr

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<210> 76

<211> 19

<212> PRT

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<223> peptide tryptic fragment H-T1-2

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